

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/816,011DATE: 10/27/97
TIME: 16:05:00

INPUT SET: S21197.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

4 7R
11/04/97

SEQUENCE LISTING

ENTERED

1
2
3 (1) General Information:
4
5 (i) APPLICANT: Price, Laura A.
6 Pausch, Mark H.
7
8 (ii) TITLE OF INVENTION: Potassium Channels, Nucleotide Sequences
9 Encoding Them, and Methods of Using Same
10
11 (iii) NUMBER OF SEQUENCES: 56
12
13 (iv) CORRESPONDENCE ADDRESS:
14 (A) ADDRESSEE: American Home Products Corporation
15 (B) STREET: One Campus Drive
16 (C) CITY: Parsippany
17 (D) STATE: New Jersey
18 (E) COUNTRY: USA
19 (F) ZIP: 07054
20
21 (v) COMPUTER READABLE FORM:
22 (A) MEDIUM TYPE: Floppy disk
23 (B) COMPUTER: IBM PC compatible
24 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
25 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
26
27 (vi) CURRENT APPLICATION DATA:
28 (A) APPLICATION NUMBER: US
29 (B) FILING DATE: 11-MAR-1997
30 (C) CLASSIFICATION:
31
32 (viii) ATTORNEY/AGENT INFORMATION:
33 (A) NAME: Matthews, Gale F.
34 (B) REGISTRATION NUMBER: 32,269
35 (C) REFERENCE/DOCKET NUMBER: 32,421-C2
36
37 (ix) TELECOMMUNICATION INFORMATION:
38 (A) TELEPHONE: 201-683-2134
39 (B) TELEFAX: 201-683-4117
40
41
42 (2) INFORMATION FOR SEQ ID NO:1:
43
44 (i) SEQUENCE CHARACTERISTICS:
45 (A) LENGTH: 2441 base pairs
46 (B) TYPE: nucleic acid

RAW SEQUENCE LISTING PATENT APPLICATION US/08/816,011

DATE: 10/27/97
TIME: 16:05:03

INPUT SET: S21197.raw

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47      (C) STRANDEDNESS: single
48      (D) TOPOLOGY: linear
49
50
51
52      (ix) FEATURE:
53          (A) NAME/KEY: CDS
54          (B) LOCATION: 190..2043
55
56
57      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
58
59      ACGCGATCGC CGCGAGTGTA TATTTTTTTTTT TTAGCTCAGT CTTTCAGTGTT TCGCGATTCT      60
60
61      CTTTAAAAGA AAAAAAAAAAT AATAAGTCAA AACTACAAAC CACACAGCGA AAGGCGAAAG      120
62
63      CAACGGTTCC TGCAGAGTGTT TATTTTTTTTTT TTCAACAATT TTTGATCGTA GTGCGACAAT      180
64
65      CCGTCGAGC ATG TCG CCG AAT CGA TGG ATC CTG CTG CTC ATC TTC TAC      228
66      Met Ser Pro Asn Arg Trp Ile Leu Leu Leu Ile Phe Tyr
67      1 5 10
68
69      ATA TCC TAC CTG ATG TTC GGG GCG GCA ATC TAT TAC CAT ATT GAG CAC      276
70      Ile Ser Tyr Leu Met Phe Gly Ala Ala Ile Tyr Tyr His Ile Glu His
71      15 20 25
72
73      GGC GAG GAG AAG ATA TCG CGC GCC GAA CAG CGC AAG GCG CAA ATT GCA      324
74      Gly Glu Glu Lys Ile Ser Arg Ala Glu Gln Arg Lys Ala Gln Ile Ala
75      30 35 40 45
76
77      ATC AAC GAA TAT CTG CTG GAG GAG CTG GGC GAC AAG AAT ACG ACC ACA      372
78      Ile Asn Glu Tyr Leu Leu Glu Glu Leu Gly Asp Lys Asn Thr Thr Thr
79      50 55 60
80
81      CAG GAT GAG ATT CTT CAA CGG ATC TCG GAT TAC TGT GAC AAA CCG GTT      420
82      Gln Asp Glu Ile Leu Gln Arg Ile Ser Asp Tyr Cys Asp Lys Pro Val
83      65 70 75
84
85      ACA TTG CCG CCG ACA TAT GAT GAT ACG CCC TAC ACG TGG ACC TTC TAC      468
86      Thr Leu Pro Pro Thr Tyr Asp Asp Thr Pro Tyr Thr Trp Thr Phe Tyr
87      80 85 90
88
89      CAT GCC TTC TTC TTC GCC TTC ACC GTT TGC TCC ACG GTG GGA TAT GGG      516
90      His Ala Phe Phe Phe Ala Phe Thr Val Cys Ser Thr Val Gly Tyr Gly
91      95 100 105
92
93      AAT ATA TCG CCA ACC ACC TTC GCC GGA CGG ATG ATC ATG ATC GCG TAT      564
94      Asn Ile Ser Pro Thr Thr Phe Ala Gly Arg Met Ile Met Ile Ala Tyr
95      110 115 120 125
96
97      TCG GTG ATT GGC ATC CCC GTC AAT GGT ATC CTC TTT GCC GGC CTC GGC      612
98      Ser Val Ile Gly Ile Pro Val Asn Gly Ile Leu Phe Ala Gly Leu Gly
99      130 135 140

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DATE: 10/27/97
TIME: 16:05:07

100																	
101	GAA	TAC	TTT	GGA	CGT	ACG	TTT	GAA	GCG	ATC	TAC	AGA	CGC	TAC	AAA	AAG	660
102	Glu	Tyr	Phe	Gly	Arg	Thr	Phe	Glu	Ala	Ile	Tyr	Arg	Arg	Tyr	Lys	Lys	
103				145					150					155			
104																	
105	TAC	AAG	ATG	TCC	ACG	GAT	ATG	CAC	TAT	GTC	CCG	CCG	CAG	CTG	GGA	TTG	708
106	Tyr	Lys	Met	Ser	Thr	Asp	Met	His	Tyr	Val	Pro	Pro	Gln	Leu	Gly	Leu	
107			160					165					170				
108																	
109	ATC	ACC	ACG	GTG	GTG	ATT	GCC	CTG	ATT	CCG	GGA	ATA	GCT	CTC	TTC	CTG	756
110	Ile	Thr	Thr	Val	Val	Ile	Ala	Leu	Ile	Pro	Gly	Ile	Ala	Leu	Phe	Leu	
111		175					180					185					
112																	
113	GTG	CTG	CCC	TGC	GTG	GGT	GTT	CAC	CTA	CTT	CGA	GAA	CTG	GGC	CTA	TCT	804
114	Val	Leu	Pro	Cys	Val	Gly	Val	His	Leu	Leu	Arg	Glu	Leu	Gly	Leu	Ser	
115	190					195					200					205	
116																	
117	TCC	ATC	TCG	CTG	TAC	TAC	AGC	TAT	GTG	ACC	ACC	ACA	ACA	ATT	GGA	TTC	852
118	Ser	Ile	Ser	Leu	Tyr	Tyr	Ser	Tyr	Val	Thr	Thr	Thr	Thr	Ile	Gly	Phe	
119					210					215					220		
120																	
121	GGT	GAC	TAT	GTG	CCC	ACA	TTT	GGA	GCC	AAC	CAG	CCC	AAG	GAG	TTC	GGC	900
122	Gly	Asp	Tyr	Val	Pro	Thr	Phe	Gly	Ala	Asn	Gln	Pro	Lys	Glu	Phe	Gly	
123				225					230					235			
124																	
125	GGC	TGG	TTC	GTG	GTC	TAT	CAG	ATC	TTT	GTG	ATC	GTG	TGG	TTC	ATC	TTC	948
126	Gly	Trp	Phe	Val	Val	Tyr	Gln	Ile	Phe	Val	Ile	Val	Trp	Phe	Ile	Phe	
127		240						245					250				
128																	
129	TCG	CTG	GGA	TAT	CTT	GTG	ATG	ATC	ATG	ACA	TTT	ATC	ACT	CGG	GGC	CTC	996
130	Ser	Leu	Gly	Tyr	Leu	Val	Met	Ile	Met	Thr	Phe	Ile	Thr	Arg	Gly	Leu	
131		255					260					265					
132																	
133	CAG	AGC	AAG	AAG	CTG	GCA	TAC	CTG	GAG	CAG	CAG	TTG	TCC	TCC	AAC	CTG	1044
134	Gln	Ser	Lys	Lys	Leu	Ala	Tyr	Leu	Glu	Gln	Gln	Leu	Ser	Ser	Asn	Leu	
135	270					275					280					285	
136																	
137	AAG	GCC	ACA	CAG	AAT	CGC	ATC	TGG	TCT	GGC	GTC	ACC	AAG	GAT	GTG	GGC	1092
138	Lys	Ala	Thr	Gln	Asn	Arg	Ile	Trp	Ser	Gly	Val	Thr	Lys	Asp	Val	Gly	
139																	

RAW SEQUENCE LISTING PATENT APPLICATION US/08/816,011

DATE: 10/27/97
TIME: 16:05:11

INPUT SET: S21197.raw

153	CGG AAG AGG GCA TTC TCC GTG TGC GCC GAC ATG GTT GGC GCC CAA AGG	1284
154	Arg Lys Arg Ala Phe Ser Val Cys Ala Asp Met Val Gly Ala Gln Arg	
155	350 355 360 365	
156		
157	GAG GCG GGC ATG GTA CAC GCC AAT TCC GAT ACG GAT CTA ACC AAA CTG	1332
158	Glu Ala Gly Met Val His Ala Asn Ser Asp Thr Asp Leu Thr Lys Leu	
159	370 375 380	
160		
161	GAT CGC GAG AAG ACA TTC GAG ACG GCG GAG GCG TAC CAC CAG ACC ACC	1380
162	Asp Arg Glu Lys Thr Phe Glu Thr Ala Glu Ala Tyr His Gln Thr Thr	
163	385 390 395	
164		
165	GAT TTG CTG GCC AAG GTG GTC AAC GCA CTG GCC ACG GTG AAG CCA CCG	1428
166	Asp Leu Leu Ala Lys Val Val Asn Ala Leu Ala Thr Val Lys Pro Pro	
167	400 405 410	
168		
169	CCG GCG GAA CAG GAA GAT GCG GCT CTC TAT GGT GGC TAT CAT GGC TTC	1476
170	Pro Ala Glu Gln Glu Asp Ala Ala Leu Tyr Gly Gly Tyr His Gly Phe	
171	415 420 425	
172		
173	TCC GAC TCC CAG ATC CTG GCC AGC GAA TGG TCG TTC TCG ACG GTC AAC	1524
174	Ser Asp Ser Gln Ile Leu Ala Ser Glu Trp Ser Phe Ser Thr Val Asn	
175	430 435 440 445	
176		
177	GAG TTC ACA TCA CCG CGA CGT CCA AGA GCA CGT GCC TGC TCC GAT TTC	1572
178	Glu Phe Thr Ser Pro Arg Arg Pro Arg Ala Arg Ala Cys Ser Asp Phe	
179	450 455 460	
180		
181	AAT CTG GAG GCA CCT CGC TGG CAG AGC GAG AGG CCA CTG CGT TCG AGC	1620
182	Asn Leu Glu Ala Pro Arg Trp Gln Ser Glu Arg Pro Leu Arg Ser Ser	
183	465 470 475	
184		
185	CAC AAC GAA TGG ACA TGG AGC GGC GAC AAC CAG CAG ATC CAG GAG GCA	1668
186	His Asn Glu Trp Thr Trp Ser Gly Asp Asn Gln Gln Ile Gln Glu Ala	
187	480 485 490	
188		
189	TTC AAC CAG CGC TAC AAG GGA CAG CAG CGT GCC AAC GGA GCA GCC AAC	1716
190	Phe Asn Gln Arg Tyr Lys Gly Gln Gln Arg Ala Asn Gly Ala Ala Asn	
191	495 500 505	
192		
193	TCG ACC ATG GTC CAT CTG GAG CCG GAT GCT TTG GAG GAG CAG CTG AGA	1764
194	Ser Thr Met Val His Leu Glu Pro Asp Ala Leu Glu Glu Gln Leu Arg	
195	510 515 520 525	
196		
197	AAC AAT CAC CGG GTG CCG GTC GCG TCA AGA AGT TCT CCA TGC CGG ATG	1812
198	Asn Asn His Arg Val Pro Val Ala Ser Arg Ser Ser Pro Cys Arg Met	
199	530 535 540	
200		
201	GTC TGC GAC GTC TGT TTC CCT TCC AGA AGA AGC ACC CCT CGC AGG ATC	1860
202	Val Cys Asp Val Cys Phe Pro Ser Arg Arg Ser Thr Pro Arg Arg Ile	
203	545 550 555	
204		
205	TGG AGC GCA AGT TGT CCG TGG TCT CGG TAC CCG AGG GTG TCA TCT CGC	1908

RAW SEQUENCE LISTING PATENT APPLICATION US/08/816,011

DATE: 10/27/97
TIME: 16:05:15

INPUT SET: S21197.raw

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206 Trp Ser Ala Ser Cys Pro Trp Ser Arg Tyr Pro Arg Val Ser Ser Arg
207      560      565      570
208
209 AGG AAG CCA GAT CCC CGC TGG ACT ACT ACA TCA ACA CGG TCA CGG CGG      1956
210 Arg Lys Pro Asp Pro Arg Trp Thr Thr Thr Ser Thr Arg Ser Arg Arg
211      575      580      585
212
213 CCT CCA GTC AAT CCT ATT TGC GCA ACG GAC GCG GTC CGC CAC CGC CCT      2004
214 Pro Pro Val Asn Pro Ile Cys Ala Thr Asp Ala Val Arg His Arg Pro
215      590      595      600      605
216
217 TCG AAT CGA ATG GCA GCT TGG CCA GCG GCG GCG GCG GGC TAACGAACAT      2053
218 Ser Asn Arg Met Ala Ala Trp Pro Ala Ala Ala Gly
219      610      615
220
221 GGGCTTCCAG ATGGAGGATG GAGCAACCCC GCCATCGGCA TTGGGCGGTG GAGCCTATCA      2113
222
223 ACGCAAGGCG GCTGCTGGCA AGCGCCGACG CGAGAGCATC TACACCCAGA ATCAAGCCCC      2173
224
225 ATCCGCTCGC CGGGGCAGCA TGTATCCGCC GACCGCGCAC GCCTTGGCCC AGATGCAGAT      2233
226
227 GCGACGCGGC AGCTTGGCAA CCAGTGGCTC TGGATCGGCG GCCATGGCGG CAGTGGCCGC      2293
228
229 GCGTCGTGGC AGCCTCTTCC CAGCTACAGC ATCGGCATCA TCGCTGACCT CTGCTCCGCG      2353
230
231 CCGAAGCAGC ATATTCTCGG TTACCTCCGA AAAGGATATG AATGTGCTGG AGCAGACGAC      2413
232
233 CATTGCGGAT CTGATTCGTG CGCTCGAG      2441
234
235

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(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 618 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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247 Met Ser Pro Asn Arg Trp Ile Leu Leu Leu Ile Phe Tyr Ile Ser Tyr
248      1      5      10      15
249
250 Leu Met Phe Gly Ala Ala Ile Tyr Tyr His Ile Glu His Gly Glu Glu
251      20      25      30
252
253 Lys Ile Ser Arg Ala Glu Gln Arg Lys Ala Gln Ile Ala Ile Asn Glu
254      35      40      45
255
256 Tyr Leu Leu Glu Glu Leu Gly Asp Lys Asn Thr Thr Thr Gln Asp Glu
257      50      55      60
258

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PAGE: 1

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/08/816,011

DATE: 10/27/97
TIME: 16:05:19

INPUT SET: S21197.raw

Line	Error	Original Text
28	Wrong application Serial Number	(A) APPLICATION NUMBER: US